

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Dalla-Favera, Riccardo
Chaganti, Raju S.K.
- (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: United States of America
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
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 - (A) TELEPHONE: (212) 278-0400
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 328..2445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCCTCGA GCCTCGAACC GGAACCTCCA AATCCGAGAC GCTCTGCTTA TGAGGACCTC	60
GAAATATGCC GGCCAGTGAA AAAATCTTAT GGCTTTGAGG GCTTTTGGTT GGCCAGGGGC	120

AGTAAAAATC TCGGAGAGCT GACACCAAGT CCTCCCCTGC CACGTAGCAG TGGTAAAGTC	180
CGAAGCTCAA ATTCCGAGAA TTGAGCTCTG TTGATTCTTA GAACTGGGGT TCTTAGAAGT	240
GGTGATGCAA GAAGTTTCTA GGAAAGGCCG GACACCAGGT TTTGAGCAAA ATTTTGGACT	300
GTGAAGCAAG GCATTGGTGA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT	351
Met Ala Ser Pro Ala Asp Ser Cys	
1 5	
ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT	399
Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg	
10 15 20	
CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT	447
Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg	
25 30 35 40	
GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG	495
Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu	
45 50 55	
TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC	543
Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile	
60 65 70	
AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC	591
Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp	
75 80 85	
TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT	639
Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala	
90 95 100	
GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT	687
Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr	
105 110 115 120	
TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC	735
Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile	
125 130 135	
AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA	783
Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln	
140 145 150	
GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA	831
Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro	
155 160 165	
CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG	879
Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu	
170 175 180	
TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC	927
Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His	
185 190 195 200	
CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC	975
Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val	
205 210 215	

CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT	1023
Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys	
220 225 230	
GAT AGT GCC AGG CCA GTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG	1071
Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu	
235 240 245	
GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA	1119
Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr	
250 255 260	
ATC CCA GAA GAG GCA CGA AGT GAT ATG CAC TAC AGT GTG GCT GAG GGC	1167
Ile Pro Glu Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Gly	
265 270 275 280	
CTC AAA CCT GCT GCC CCC TCA GCC CGA AAT GCC CCC TAC TTC CCT TGT	1215
Leu Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys	
285 290 295	
GAC AAG GCC AGC AAA GAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT	1263
Asp Lys Ala Ser Lys Glu Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile	
300 305 310	
GCC CTG CAT TTC GAG CCC CCC AAT GCA CCC CTG AAC CGG AAG GGT CTG	1311
Ala Leu His Phe Glu Pro Pro Asn Ala Pro Leu Asn Arg Lys Gly Leu	
315 320 325	
GTT AGT CCA CAG AGC CCC CAG AAA TCT GAC TGC CAG CCC AAC TCG CCC	1359
Val Ser Pro Gln Ser Pro Gln Lys Ser Asp Cys Gln Pro Asn Ser Pro	
330 335 340	
ACA GAG GCC TGC AGC AGT AAG AAT GCC TGC ATC CTC CAG GGT TCT GGC	1407
Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Gln Gly Ser Gly	
345 350 355 360	
TCC CCT CCA GCC AAG AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AAG	1455
Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Trp Lys	
365 370 375	
AAA TAC AAG TTC ATC GTG CTC AAC AGC CTC AAC CAG AAT GCC AAA CCA	1503
Lys Tyr Lys Phe Ile Val Leu Asn Ser Leu Asn Gln Asn Ala Lys Pro	
380 385 390	
GGG GGG CCT GAG CAG GCT GAG CTG GGC CGC CTT TCC CCA CGA GCC TAC	1551
Gly Gly Pro Glu Gln Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr	
395 400 405	
ACG GCC CCA CCT GCC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTT GAC	1599
Thr Ala Pro Pro Ala Cys Gln Pro Pro Met Glu Pro Glu Asn Leu Asp	
410 415 420	
CTC CAG TCC CCA ACC AAG CTG AGT GCC AGC GGG GAG GAC TCC ACC ATC	1647
Leu Gln Ser Pro Thr Lys Leu Ser Ala Ser Gly Glu Asp Ser Thr Ile	
425 430 435 440	
CCA CAA GCC AGC CGG CTC AAT AAC ATC GTT AAC AGG TCC ATG ACG GGC	1695
Pro Gln Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly	
445 450 455	
TCT CCC CGC AGC AGC AGC GAG AGC CAC TCA CCA CTC TAC ATG CAC CCC	1743
Ser Pro Arg Ser Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro	

[illegible]

CTTTCGTCTC	CAGCCCCCTC	TCAGAATCTA	CCCAAAGGAT	ACTGTAACAC	TTTACAATGT	2525
TCATCCCATG	ATGTAGTGCC	TCTTTCATCC	ACTAGTGCAA	ATCATAGCTG	GGGGTTGGGG	2585
GTGGTGGGGG	TCGGGGCCTG	GGGGACTGGG	AGCCGCAGCA	GCTCCCCCTC	CCCCACTGCC	2645
ATAAAACATT	AAGAAAATCA	TATTGCTTCT	TCTCCTATGT	GNNNNNNNNN	NNNNNNNNNN	2705
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2765
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2825
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2885
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2945
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3005
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3065
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3125
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3185
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3245
NTTTAAGTAT	TGCATCTGTA	TAAGTAAGAA	AATATTTTGT	CTAAAATGCC	TCAGTGTATT	3305
TGTATTTTTT	TGCAAGTGGG	GGGTTACAAT	TTACCCAGTG	TGTATTAAAA	AAAACCCAAA	3365
GAACCCAAAA	ATCTCCAGAA	GGAAAAATGT	GTAATTTTGT	TCTAGTTTTT	AGTTTGTATA	3425
TACCCGTACA	ACGTGTCCTC	ACGGTGCCTT	TTTTCACGGA	AGTTTTCAAT	GATGGGCGAG	3485
CGTGCACCAT	CCCTTTTTGA	AGTGTAGGCA	GACACAGGGA	CTTGAAGTTG	TTACTAACTA	3545
AACTCTCTTT	GGGAATGTTT	GTCTCATCCC	ANTCTGCGTC	ATGCTTGTGT	GATAACTACT	3605
CCGAGACAG	GGTTTGGCTG	TGTCTAAACT	GCATTACCGC	GTTGTAAAAA	ATAGCTGTAC	3665
CAATATAAGA	ATAAAATGTT	GGAAAGTCGC	AAAAAAAAAA	AAAAAAAAAA	AAAAA	3720

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Pro	Ala	Asp	Ser	Cys	Ile	Gln	Phe	Thr	Arg	His	Ala	Arg
1				5					10					15	
Asp	Val	Leu	Leu	Asn	Leu	Asn	Arg	Leu	Arg	Ser	Arg	Asp	Ile	Leu	Thr
		20						25					30		
Asp	Val	Val	Ile	Val	Val	Ser	Arg	Glu	Gln	Phe	Arg	Ala	His	Lys	Thr
		35						40				45			

Val	Leu	Met	Ala	Trp	Arg	Gly	Leu	Phe	Tyr	Ser	Ile	Phe	Thr	Asp	Gln
50						55					60				
Leu	Lys	Cys	Asn	Leu	Ser	Val	Ile	Asn	Leu	Asp	Pro	Glu	Ile	Asn	Pro
65					70					75					80
Glu	Gly	Phe	Cys	Ile	Leu	Leu	Asp	Phe	Met	Tyr	Thr	Ser	Arg	Leu	Asn
				85					90					95	
Leu	Arg	Glu	Gly	Asn	Ile	Met	Ala	Val	Met	Ala	Thr	Ala	Met	Tyr	Leu
			100					105					110		
Gln	Met	Glu	His	Val	Val	Asp	Thr	Cys	Arg	Lys	Phe	Ile	Lys	Ala	Ser
		115					120					125			
Glu	Ala	Glu	Met	Val	Ser	Ala	Ile	Lys	Pro	Pro	Arg	Glu	Glu	Phe	Leu
	130					135					140				
Asn	Ser	Arg	Met	Leu	Met	Pro	Gln	Asp	Ile	Met	Ala	Tyr	Arg	Gly	Arg
145					150					155					160
Glu	Val	Val	Glu	Asn	Asn	Leu	Pro	Leu	Arg	Ser	Ala	Pro	Gly	Cys	Glu
				165				170						175	
Ser	Arg	Ala	Phe	Ala	Pro	Ser	Leu	Tyr	Ser	Gly	Leu	Ser	Thr	Pro	Pro
			180					185					190		
Ala	Ser	Tyr	Ser	Met	Tyr	Ser	His	Leu	Pro	Val	Ser	Ser	Leu	Leu	Phe
		195					200					205			
Ser	Asp	Glu	Glu	Phe	Arg	Asp	Val	Arg	Met	Pro	Val	Ala	Asn	Pro	Phe
	210					215					220				
Pro	Lys	Glu	Arg	Ala	Leu	Pro	Cys	Asp	Ser	Ala	Arg	Pro	Val	Pro	Gly
225					230					235					240
Glu	Tyr	Ser	Arg	Pro	Thr	Leu	Glu	Val	Ser	Pro	Asn	Val	Cys	His	Ser
				245					250					255	
Asn	Ile	Tyr	Ser	Pro	Lys	Glu	Thr	Ile	Pro	Glu	Glu	Ala	Arg	Ser	Asp
			260					265					270		
Met	His	Tyr	Ser	Val	Ala	Glu	Gly	Leu	Lys	Pro	Ala	Ala	Pro	Ser	Ala
		275					280					285			
Arg	Asn	Ala	Pro	Tyr	Phe	Pro	Cys	Asp	Lys	Ala	Ser	Lys	Glu	Glu	Glu
	290					295					300				
Arg	Pro	Ser	Ser	Glu	Asp	Glu	Ile	Ala	Leu	His	Phe	Glu	Pro	Pro	Asn
305					310					315					320
Ala	Pro	Leu	Asn	Arg	Lys	Gly	Leu	Val	Ser	Pro	Gln	Ser	Pro	Gln	Lys
				325					330					335	
Ser	Asp	Cys	Gln	Pro	Asn	Ser	Pro	Thr	Glu	Ala	Cys	Ser	Ser	Lys	Asn
			340					345					350		
Ala	Cys	Ile	Leu	Gln	Gly	Ser	Gly	Ser	Pro	Pro	Ala	Lys	Ser	Pro	Thr
		355					360					365			
Asp	Pro	Lys	Ala	Cys	Ser	Trp	Lys	Lys	Tyr	Lys	Phe	Ile	Val	Leu	Asn

$\begin{array}{c} \text{---} \\ | \\ \text{---} \end{array}$

Ala Cys
705

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Gly Ser Phe Val Gln His Ser Val Arg Val Leu Gln Glu Leu Asn
 1 5 10 15
 Lys Gln Arg Glu Lys Gly Gln Tyr Cys Asp Ala Thr Leu Asp Val Gly
 20 25 30
 Gly Leu Val Phe Lys Ala His Trp Ser Val Leu Ala Cys Cys Ser His
 35 40 45
 Phe Phe Gln Ser Leu Tyr Gly Asp Gly Ser Gly Gly Ser Val Val Leu
 50 55 60
 Pro Ala Gly Phe Ala Glu Ile Phe Gly Leu Leu Leu Asp Phe Phe Tyr
 65 70 75 80
 Thr Gly His Leu Ala Leu Thr Ser Gly Asn Arg Asp Gln Val Leu Leu
 85 90 95
 Ala Ala Arg Glu Leu Arg Val
 100

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Ala Ser His Ser Leu Val Leu Leu Gln Gln Leu Asn Met
 1 5 10 15
 Gln Arg Glu Phe Gly Phe Leu Cys Asp Cys Thr Val Ala Ile Gly Asp
 20 25 30

Val Tyr Phe Lys Ala His Arg Ala Val Leu Ala Ala Phe Ser Asn Tyr
 35 40 45
 Phe Lys Met Ile Phe Ile His Gln Thr Ser Glu Cys Ile Lys Ile Gln
 50 55 60
 Pro Thr Asp Ile Gln Pro Asp Ile Phe Ser Tyr Leu Leu His Ile Met
 65 70 75 80
 Tyr Thr Gly Lys Gly Pro Lys Gln Ile Val Asp His Ser Arg Leu Glu
 85 90 95
 Glu Gly Ile Arg Phe Leu His Ala Asp Tyr Leu
 100 105

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Ser Ser Glu Leu Ile Ala Val Ile Asn Gly Phe Arg Asn
 1 5 10 15
 Ser Gly Arg Phe Cys Asp Ile Ser Ile Val Ile Asn Asp Glu Arg Ile
 20 25 30
 Asn Ala His Lys Leu Ile Leu Ser Gly Ala Ser Glu Tyr Phe Ser Ile
 35 40 45
 Leu Phe Ser Asn Asn Phe Ile Asp Ser Asn Glu Tyr Glu Val Asn Leu
 50 55 60
 Ser His Leu Asp Tyr Gln Ser Val Asn Asp Leu Ile Asp Tyr Ile Tyr
 65 70 75 80
 Gly Ile Pro Leu Ser Leu Thr Asn Asp Asn Val Lys Tyr Ile Leu Ser
 85 90 95
 Thr Ala Asp Phe Leu Gln Ile Gly Ser Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Leu	Arg	Trp	Asn	Asn	His	Gln	Ser	Asn	Leu	Leu	Ser	Val	Phe	Asp
1				5					10					15	
Gln	Leu	Leu	His	Ala	Glu	Thr	Phe	Thr	Asp	Val	Thr	Leu	Ala	Val	Glu
			20					25					30		
Gly	Gln	His	Leu	Lys	Ala	His	Lys	Asn	Val	Leu	Ser	Ala	Cys	Ser	Pro
		35					40					45			
Tyr	Phe	Asn	Thr	Leu	Phe	Val	Ser	His	Pro	Glu	Lys	His	Pro	Ile	Val
	50					55					60				
Ile	Leu	Lys	Asp	Val	Pro	Tyr	Ser	Asp	Met	Lys	Ser	Leu	Leu	Asp	Phe
65					70					75					80
Met	Tyr	Arg	Gly	Glu	Val	Ser	Val	Asp	Gln	Glu	Arg	Leu	Thr	Ala	Phe
			85						90					95	
Leu	Arg	Val	Ala	Glu	Ser	Leu	Arg	Ile	Lys	Gly	Leu				
			100					105							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln	Tyr	Ser	Asn	Glu	Gln	His	Thr	Ala	Arg	Ser	Phe	Asp	Ala	Met	Asn
1				5					10					15	
Glu	Met	Arg	Lys	Gln	Lys	Gln	Leu	Cys	Asp	Val	Ile	Leu	Val	Ala	Asp
			20					25					30		
Asp	Val	Glu	Ile	His	Ala	His	Arg	Met	Val	Leu	Ala	Ser	Cys	Ser	Pro
		35					40					45			
Tyr	Phe	Tyr	Ala	Met	Phe	Thr	Ser	Phe	Glu	Glu	Ser	Arg	Gln	Ala	Arg
	50					55					60				
Ile	Thr	Leu	Gln	Ser	Val	Asp	Ala	Arg	Ala	Leu	Glu	Leu	Leu	Ile	Asp
65					70					75					80
Tyr	Val	Tyr	Thr	Ala	Thr	Val	Glu	Val	Asn	Glu	Asp	Asn	Val	Gln	Val
			85						90					95	
Leu	Leu	Thr	Ala	Ala	Asn	Leu	Leu	Gln	Leu	Thr	Asp	Val			
			100					105							

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Leu Gln Asn Pro Ser His Pro Thr Gly Leu Leu Cys Lys Ala Asn
 1 5 10 15
 Gln Met Arg Leu Ala Gly Thr Leu Cys Asp Val Val Ile Met Val Asp
 20 25 30
 Ser Gln Glu Phe His Ala His Arg Thr Val Leu Ala Cys Thr Ser Lys
 35 40 45
 Met Phe Glu Ile Leu Phe His Arg Asn Ser Gln His Tyr Thr Leu Asp
 50 55 60
 Phe Leu Ser Pro Lys Thr Phe Gln Gln Ile Leu Glu Tyr Ala Tyr Thr
 65 70 75 80
 Ala Thr Leu Gln Ala Lys Ala Glu Asp Leu Asp Asp Leu Leu Tyr Ala
 85 90 95
 Ala Glu Ile Leu Glu Ile Glu Tyr Leu
 100 105

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Leu Gln Phe Thr Arg His Ala Ser Asp Val Leu Leu Asn Leu Asn
 1 5 10 15
 Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser
 20 25 30
 Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Cys Ser Gly
 35 40 45
 Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val
 50 55 60

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Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu
65 70 75 80
Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met
85 90 95
Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val
100 105 110

110
105
100
95
90
85
80
75
70
65